

SEQUENCE LISTING

<110> Japan Science and Technology Agency

<120> Transcriptional regulator ZHX3

<130> FS03-323PCT

<160> 35

<170> PatentIn version 3.1

<210> 1

<211> 956

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Ser Lys Arg Lys Ser Thr Thr Pro Cys Met Ile Pro Val Lys

1 5 10 15

Thr Val Val Leu Gln Asp Ala Ser Met Glu Ala Gln Pro Ala Glu Thr

20 25 30

Leu Pro Glu Gly Pro Gln Gln Asp Leu Pro Pro Glu Ala Ser Ala Ala

35 40 45

Ser Ser Glu Ala Ala Gln Asn Pro Ser Ser Thr Asp Gly Ser Thr Leu

50 55 60

Ala Asn Gly His Arg Ser Thr Leu Asp Gly Tyr Leu Tyr Ser Cys Lys

65 70 75 80

Tyr Cys Asp Phe Arg Ser His Asp Met Thr Gln Phe Val Gly His Met

85 90 95

Asn Ser Glu His Thr Asp Phe Asn Lys Asp Pro Thr Phe Val Cys Ser

100 105 110

Gly Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn

115 120 125

Ala Thr Cys His Ser Gly Glu Ala Ser Phe Val Trp Asn Val Ala Lys

130 135 140

Pro Asp Asn His Val Val Val Glu Gln Ser Ile Pro Glu Ser Thr Ser

145 150 155 160

Thr Pro Asp Leu Ala Gly Glu Pro Ser Ala Glu Gly Ala Asp Gly Gln

165 170 175

Ala Glu Ile Ile Ile Thr Lys Thr Pro Ile Met Lys Ile Met Lys Gly

180 185 190

Lys Ala Glu Ala Lys Lys Ile His Thr Leu Lys Glu Asn Val Pro Ser

195 200 205

Gln Pro Val Gly Glu Ala Leu Pro Lys Leu Ser Thr Gly Glu Met Glu

210 215 220

Val Arg Glu Gly Asp His Ser Phe Ile Asn Gly Ala Val Pro Val Ser

225 230 235 240

Gln Ala Ser Ala Ser Ser Ala Lys Asn Pro His Ala Ala Asn Gly Pro

245 250 255

Leu Ile Gly Thr Val Pro Val Leu Pro Ala Gly Ile Ala Gln Phe Leu

260 265 270

Ser Leu Gln Gln Gln Pro Pro Val His Ala Gln His His Val His Gln

275 280 285

Pro Leu Pro Thr Ala Lys Ala Leu Pro Lys Val Met Ile Pro Leu Ser

290 295 300

Ser Ile Pro Thr Tyr Asn Ala Ala Met Asp Ser Asn Ser Phe Leu Lys

305 310 315 320

Asn Ser Phe His Lys Phe Pro Tyr Pro Thr Lys Ala Glu Leu Cys Tyr

325 330 335

Leu Thr Val Val Thr Lys Tyr Pro Glu Glu Gln Leu Lys Ile Trp Phe

340 345 350

Thr Ala Gln Arg Leu Lys Gln Gly Ile Ser Trp Ser Pro Glu Glu Ile

355 360 365

Glu Asp Ala Arg Lys Lys Met Phe Asn Thr Val Ile Gln Ser Val Pro

370 375 380
Gln Pro Thr Ile Thr Val Leu Asn Thr Pro Leu Val Ala Ser Ala Gly
385 390 395 400
Asn Val Gln His Leu Ile Gln Ala Ala Leu Pro Gly His Val Val Gly
405 410 415
Gln Pro Glu Gly Thr Gly Gly Gly Leu Leu Val Thr Gln Pro Leu Met
420 425 430
Ala Asn Gly Leu Gln Ala Thr Ser Ser Pro Leu Pro Leu Thr Val Thr
435 440 445
Ser Val Pro Lys Gln Pro Gly Val Ala Pro Ile Asn Thr Val Cys Ser
450 455 460
Asn Thr Thr Ser Ala Val Lys Val Val Asn Ala Ala Gln Ser Leu Leu
465 470 475 480
Thr Ala Cys Pro Ser Ile Thr Ser Gln Ala Phe Leu Asp Ala Ser Ile
485 490 495
Tyr Lys Asn Lys Lys Ser His Glu Gln Leu Ser Ala Leu Lys Gly Ser
500 505 510
Phe Cys Arg Asn Gln Phe Pro Gly Gln Ser Glu Val Glu His Leu Thr
515 520 525
Lys Val Thr Gly Leu Ser Thr Arg Glu Val Arg Lys Trp Phe Ser Asp
530 535 540
Arg Arg Tyr His Cys Arg Asn Leu Lys Gly Ser Arg Ala Met Ile Pro
545 550 555 560
Gly Asp His Ser Ser Ile Ile Ile Asp Ser Val Pro Glu Val Ser Phe
565 570 575
Ser Pro Ser Ser Lys Val Pro Glu Val Thr Cys Ile Pro Thr Thr Ala
580 585 590
Thr Leu Ala Thr His Pro Ser Ala Lys Arg Gln Ser Trp His Gln Thr
595 600 605

Pro Asp Phe Thr Pro Thr Lys Tyr Lys Glu Arg Ala Pro Glu Gln Leu

610

615

620

Arg Ala Leu Glu Ser Ser Phe Ala Gln Asn Pro Leu Pro Leu Asp Glu

625

630

635

640

Glu Leu Asp Arg Leu Arg Ser Glu Thr Lys Met Thr Arg Arg Glu Ile

645

650

655

Asp Ser Trp Phe Ser Glu Arg Arg Lys Lys Val Asn Ala Glu Glu Thr

660

665

670

Lys Lys Ala Glu Glu Asn Ala Ser Gln Glu Glu Glu Glu Ala Ala Glu

675

680

685

Asp Glu Gly Gly Glu Glu Asp Leu Ala Ser Glu Leu Arg Val Ser Gly

690

695

700

Glu Asn Gly Ser Leu Glu Met Pro Ser Ser His Ile Leu Ala Glu Arg

705

710

715

720

Lys Val Ser Pro Ile Lys Ile Asn Leu Lys Asn Leu Arg Val Thr Glu

725

730

735

Ala Asn Gly Arg Asn Glu Ile Pro Gly Leu Gly Ala Cys Asp Pro Glu

740

745

750

Asp Asp Glu Ser Asn Lys Leu Ala Glu Gln Leu Pro Gly Lys Val Ser

755

760

765

Cys Lys Lys Thr Ala Gln Gln Arg His Leu Leu Arg Gln Leu Phe Val

770

775

780

Gln Thr Gln Trp Pro Ser Asn Gln Asp Tyr Asp Ser Ile Met Ala Gln

785

790

795

800

Thr Gly Leu Pro Arg Pro Glu Val Val Arg Trp Phe Gly Asp Ser Arg

805

810

815

Tyr Ala Leu Lys Asn Gly Gln Leu Lys Trp Tyr Glu Asp Tyr Lys Arg

820

825

830

Gly Asn Phe Pro Pro Gly Leu Leu Val Ile Ala Pro Gly Asn Arg Glu

835 840 845
Leu Leu Gln Asp Tyr Tyr Met Thr His Lys Met Leu Tyr Glu Glu Asp

850 855 860
Leu Gln Asn Leu Cys Asp Lys Thr Gln Met Ser Ser Gln Gln Val Lys

865 870 875 880
Gln Trp Phe Ala Glu Lys Met Gly Glu Glu Thr Arg Ala Val Ala Asp

885 890 895
Thr Gly Ser Glu Asp Gln Gly Pro Gly Thr Gly Glu Leu Thr Ala Val

900 905 910
His Lys Gly Met Gly Asp Thr Tyr Ser Glu Val Ser Glu Asn Ser Glu

915 920 925
Ser Trp Glu Pro Arg Val Pro Glu Ala Ser Ser Glu Pro Phe Asp Thr

930 935 940
Ser Ser Pro Gln Ala Gly Arg Gln Leu Glu Thr Asp

945 950 955

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<211> 522

<212> PRT

<213> Rattus norvegicus

<400> 2

Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn Ala

1 5 10 15

Lys Cys His Ser Gly Glu Ala Ser Phe Leu Trp Asn Val Thr Lys Pro

20 25 30

Asp Asn His Val Val Val Glu Gln Ser Val Pro Glu Asn Ala Ser Ser

35 40 45

Ser Val Leu Ala Gly Glu Ser Thr Glu Gly Thr Glu Ile Ile Ile Thr

50 55 60

Lys Thr Pro Ile Met Lys Ile Met Lys Gly Lys Ala Glu Ala Lys Lys

65 70 75 80
Ile His Met Leu Lys Glu Asn Ala Pro Thr Gln Pro Gly Gly Glu Ala
85 90 95
Leu Pro Lys Pro Leu Ala Gly Glu Thr Glu Gly Lys Glu Gly Asp His
100 105 110
Thr Phe Ile Asn Gly Ala Thr Pro Val Ser Gln Ala Ser Ala Asn Ser
115 120 125
Thr Lys Pro Pro His Thr Ala Asn Gly Pro Leu Ile Gly Thr Val Pro
130 135 140
Val Leu Pro Ala Gly Ile Ala Gln Phe Leu Ser Leu Gln Gln Pro Thr
145 150 155 160
Val His Pro Gln His His Pro His Gln Pro Leu Pro Thr Ser Lys Ala
165 170 175
Leu Pro Lys Val Met Ile Pro Leu Ser Ser Ile Pro Thr Tyr Asn Ala
180 185 190
Ala Met Asp Ser Asn Ser Phe Leu Lys Asn Ser Phe His Lys Phe Pro
195 200 205
Tyr Pro Thr Lys Ala Glu Leu Cys Tyr Leu Thr Val Val Thr Lys Tyr
210 215 220
Pro Glu Glu Gln Leu Lys Ile Trp Phe Thr Ala Gln Arg Leu Lys Gln
225 230 235 240
Gly Ile Ser Trp Ser Pro Glu Glu Ile Glu Asp Ala Arg Lys Lys Met
245 250 255
Phe Asn Thr Val Ile Gln Ser Val Pro Gln Pro Thr Ile Thr Val Leu
260 265 270
Asn Thr Pro Leu Val Ala Ser Ala Gly Asn Val Gln His Leu Ile Gln
275 280 285
Ala Ala Leu Pro Gly His Ala Val Gly Gln Pro Glu Gly Thr Ala Gly
290 295 300

Gly Leu Leu Val Thr Gln Pro Leu Met Ala Asn Gly Leu Gln Ala Ser

305 310 315 320

Ser Ser Ser Leu Pro Leu Thr Thr Ala Ser Val Pro Lys Pro Thr Ala

325 330 335

Ala Pro Ile Asn Thr Val Cys Ser Asn Thr Thr Ser Ala Val Lys Val

340 345 350

Val Asn Ala Ala Gln Ser Leu Leu Thr Ala Cys Pro Ser Ile Thr Ser

355 360 365

Gln Ala Phe Leu Asp Ala Asn Ile Tyr Lys Asn Lys Lys Ser His Glu

370 375 380

Gln Leu Ser Ala Leu Lys Gly Ser Phe Cys Arg Asn Gln Phe Pro Gly

385 390 395 400

Gln Ser Glu Val Glu His Leu Thr Lys Val Thr Gly Leu Ser Thr Arg

405 410 415

Glu Val Arg Lys Trp Phe Ser Asp Arg Arg Tyr His Cys Arg Asn Leu

420 425 430

Lys Gly Thr Arg Ala Met Val Pro Gly Glu His Gly Ser Val Leu Ile

435 440 445

Asp Ser Val Pro Glu Val Pro Phe Pro Leu Ser Ser Lys Val Pro Glu

450 455 460

Val Pro Cys Val Pro Thr Ala Thr Ser Leu Val Ser His Pro Ala Thr

465 470 475 480

Lys Arg Gln Ser Trp His Gln Thr Pro Asp Phe Thr Pro Thr Lys Tyr

485 490 495

Lys Glu Arg Ala Pro Glu Gln Leu Arg Val Leu Glu Ser Ser Phe Ala

500 505 510

Gln Asn Pro Leu Pro Pro Glu Glu Glu Leu

515 520

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19

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gtggcagaca caggcagtg

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<210> 6

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ggccgcatcc cagactggcc agtcc

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cctgagcagc attccaacg

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cttcttggtc tcctcagcat tcac

24

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gtgattgtca ccatggccag

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<212> DNA

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<400> 14

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<210> 15

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<210> 18

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ccaatcatga agataatgaa aggc

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ccggggatcc tggcttgcc acgtccac

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32

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ccgggaattc acccttgat gcagtgggtg

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ccgggaattc acccttgat gcagtgggtg

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ccgggaattc acctttgtat gcagtgggtg

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<400> 33

aattccacca cactggatcc ctggtac

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ggcatcttgc aacaccacag tcttc

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catgcatggt gtggtggatt tcctc

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